

Exhibit A

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Qy	Matches	B; Conservative	0; Mismatches	O; Indels	O; Gaps	O;
223 ALASSISSV	230					
98 ALASSISSV	105					

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Query Match Score: 8; DB: 1; Length: 618;
 Best Local Similarity: 100.0%; Pred. No.: 12;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy (32+) 223 ALASISSV 230
 * Db (61+) 98 ALASISSV 105

RESULT 7
 MUTL_CHLTB STANDARD; PRT; 624 AA.
 ID MUTL_CHLTB
 AC Q8NSX3;
 DT 28-Feb-2003 (Rel. 41, Created)
 DT 28-Feb-2003 (Rel. 41, Last sequence update)
 DE DNA mismatch repair protein mutL
 GN MURY OR CTR228
 OS Chlorobium cepidum
 OC Chlorobium, Chlorobi; Chlorobiales; Chlorobiaceae;
 OC Chlorobium; Chlorobi
 OX NCBI_TAXID=1097;
 RP SEQUENCE FROM N.A.
 RX STRAIN=L-TLS / ATCC 49652 / DSM 12025;
 RA Bisen J.A., Nelson I.T., Heidelberg J.P., Wu M.,
 RA Dodson R.J., Deboy R., Gwyn M., Nelson W.C., Haft D.H.,
 RA Hickey E.X., Peterson J.D., Durkin S.E., Kolonay J.L., Yang F.,
 RA Holt I., Umayam L.A., Mason T., Brenner M., Parksey D.,
 RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
 RA Venkatesan J., Khoruri H., White O., Gruber T.M., Ketchum K.A.,
 RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,
 RT "The complete genome sequence of *Chlorobium tepidum* TLS, a
 photosynthetic, anaerobic, green-sulfur bacterium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).

.-!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity).
 .!- SIMILARITY: Belongs to the DNA mismatch repair mutL/heXL family.

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EMBL: AE012953; AAC73245.1; -.
 DR TIGR: CT20298; -.
 DR HAMAP_MP_00149; -; 1.
 DR InterPro: IPR001594; ATPbind_Atpase.
 DR InterPro: IPR002095; DNA_misRepair.
 DR PF00119; DNA_misRepair_1.
 DR PF00216; HATbase_C; 1.
 DR TIGRFAM6; TIGR00585; mutL; 1.
 DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
 DR DNA repair; Complete Proteome; 1.
 DR SEQUENCE: 624 AA; 69816 MW;

Query Match Score: 8; DB: 1; Length: 624;
 Best Local Similarity: 100.0%; Pred. No.: 12;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 223 ALASISSV 230
 * Db 99 ALASISSV 105

RESULT 8
 MUTL_HABIN STANDARD; PRT; 629 AA.
 ID P44947;
 AC P44947;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA mismatch repair protein mutL.
 GN MURY OR HIO067.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus; Haemophilus.
 OX NCBI_TAXID=727;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BD / XMM20 / ATCC 51907;
 RC MEDLINE=95310X30; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shizley R., Liu L.-I., Glodek A., Kelley J.M., Weitman J.F., Phillips C.A., Spirogs T., Hedges R., Hedblom B., Corlton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman L.L., Fuhrmann J.L., Geoghegan N.S.M., Green C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
 RA "Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd";
 RT Science 269:996-912 (1995).
 .!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. May act as a "molecular matchmaker", a protein that promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex (By similarity).
 .!- SIMILARITY: Belongs to the DNA mismatch repair mutL/heXL family.

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CC EMBL: U32692; AAC21745.1; -.
 DR PIR: B64046; B64046.
 DR HSSP: P23167; 1BKN.
 DR TIGR: HI0067; -.
 DR HAMAP_MP_00119; -.
 DR InterPro: IPR003554; ATPbind_Atpase.
 DR InterPro: IPR002059; DNA_misRepair.
 DR PF01119; DNA_misRepair_1.
 DR P02518; HATbase_C; 1.
 DR SMART: SM0097; HATbase_C; 1.
 DR TIGRFAM6; TIGR00585; mutL; 1.
 DR PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
 DR DNA repair; Complete Proteome; 1.
 DR SEQUENCE: 629 AA; 71622 MW;

Query Match Score: 8; DB: 1; Length: 629;
 Best Local Similarity: 100.0%; Pred. No.: 12;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 223 ALASISSV 230
 * Db 98 ALASISSV 105

RESULT 9
 MUTL_PSEPK STANDARD; PRT; 632 AA.
 ID Q8BD11;